

SEQUENCE LISTING

<110> Langermann, Solomon R.
Hultgren, Scott J.
Hung, Chia-Suei
Bouckaert, Julie

<120> Mutant Proteins, High Potency Inhibitory Antibodies, and FimCH
Crystal Structure

<130> 10271-037

<140>

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<160> 50

<170> PatentIn version 3.0

<210> 1

<211> 726

<212> DNA

<213> E. coli

<220>

<221> CDS

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tgc ttg ctg gca ggt atc ctg atg ttc atg gca atg atg gtt gcc gga 96

Cys Leu Leu Ala Gly Ile Leu Met Phe Met Ala Met Met Val Ala Gly
20 25 30

cgc gct gaa gcg gga gtg gcc tta ggt gcg act cgc gta att tat ccg 144

Arg Ala Glu Ala Gly Val Ala Leu Gly Ala Thr Arg Val Ile Tyr Pro
35 40 45

gca ggg caa aaa caa gtg caa ctt gcc gtg aca aat aat gat gaa aat 192

Ala Gly Gln Lys Gln Val Gln Leu Ala Val Thr Asn Asn Asp Glu Asn
50 55 60

agt acc tat tta att caa tca tgg gtg gaa aat gcc gat ggt gta aag 240

Ser Thr Tyr Leu Ile Gln Ser Trp Val Glu Asn Ala Asp Gly Val Lys
65 70 75 80

gat ggt cgt ttt atc gtg acg cct cct ctg ttt gcg atg aag gga aaa 288

Asp Gly Arg Phe Ile Val Thr Pro Pro Leu Phe Ala Met Lys Gly Lys
85 90 95

aaa gag aat acc tta cgt att ctt gat gca aca aat aac caa ttg cca 336

Lys Glu Asn Thr Leu Arg Ile Leu Asp Ala Thr Asn Asn Gln Leu Pro
100 105 110

cag gac cgg gaa agt tta ttc tgg atg aac gtt aaa gcg att ccg tca 384

Gln Asp Arg Glu Ser Leu Phe Trp Met Asn Val Lys Ala Ile Pro Ser
115 120 125

atg gat aaa tca aaa ttg act gag aat acg cta cag ctc gca att atc	432
Met Asp Lys Ser Lys Leu Thr Glu Asn Thr Leu Gln Leu Ala Ile Ile	
130 135 140	
agc cgc att aaa ctg tac tat cgc ccg gct aaa tta gcg ttg cca ccc	480
Ser Arg Ile Lys Leu Tyr Tyr Arg Pro Ala Lys Leu Ala Leu Pro Pro	
145 150 155 160	
gat cag gcc gca gaa aaa tta aga ttt cgt cgt agc gcg aat tct ctg	528
Asp Gln Ala Ala Glu Lys Leu Arg Phe Arg Arg Ser Ala Asn Ser Leu	
165 170 175	
acg ctg att aac ccg aca ccc tat tac ctg acg gta aca gag ttg aat	576
Thr Leu Ile Asn Pro Thr Pro Tyr Tyr Leu Thr Val Thr Glu Leu Asn	
180 185 190	
gcc gga acc cgg gtt ctt gaa aat gca ttg gtg cct cca atg ggc gaa	624
Ala Gly Thr Arg Val Leu Glu Asn Ala Leu Val Pro Pro Met Gly Glu	
195 200 205	
agc acg gtt aaa ttg cct tct gat gca gga agc aat att act tac cga	672
Ser Thr Val Lys Leu Pro Ser Asp Ala Gly Ser Asn Ile Thr Tyr Arg	
210 215 220	
aca ata aat gat tat ggc gca ctt acc ccc aaa atg acg ggc gta atg	720
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Glu	

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 <212> PRT
 <213> E. coli

<400> 2

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Arg Ala Glu Ala Gly Val Ala Leu Gly Ala Thr Arg Val Ile Tyr Pro	
35 40 45	
Ala Gly Gln Lys Gln Val Gln Leu Ala Val Thr Asn Asn Asp Glu Asn	
50 55 60	
Ser Thr Tyr Leu Ile Gln Ser Trp Val Glu Asn Ala Asp Gly Val Lys	
65 70 75 80	
Asp Gly Arg Phe Ile Val Thr Pro Pro Leu Phe Ala Met Lys Gly Lys	
85 90 95	
Lys Glu Asn Thr Leu Arg Ile Leu Asp Ala Thr Asn Asn Gln Leu Pro	
100 105 110	
Gln Asp Arg Glu Ser Leu Phe Trp Met Asn Val Lys Ala Ile Pro Ser	
115 120 125	
Met Asp Lys Ser Lys Leu Thr Glu Asn Thr Leu Gln Leu Ala Ile Ile	
130 135 140	
Ser Arg Ile Lys Leu Tyr Tyr Arg Pro Ala Lys Leu Ala Leu Pro Pro	
145 150 155 160	
Asp Gln Ala Ala Glu Lys Leu Arg Phe Arg Arg Ser Ala Asn Ser Leu	
165 170 175	

Thr	Leu	Ile	Asn	Pro	Thr	Pro	Tyr	Tyr	Leu	Thr	Val	Thr	Glu	Leu	Asn
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Ala	Gly	Thr	Arg	Val	Leu	Glu	Asn	Ala	Leu	Val	Pro	Pro	Met	Gly	Glu
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gta	aat	gcc	tgg	tca	ttc	gcc	tgt	aaa	acc	gcc	aat	ggc	acc	gct	atc				96
Val	Asn	Ala	Trp	Ser	Phe	Ala	Cys	Lys	Thr	Ala	Asn	Gly	Thr	Ala	Ile				
-5				-1	1				5					10					
cct	att	ggc	ggc	ggc	agc	gcc	aat	ggt	tat	gta	aac	ctt	gcg	ccc	gtc				144
Pro	Ile	Gly	Gly	Gly	Ser	Ala	Asn	Val	Tyr	Val	Asn	Leu	Ala	Pro	Val				
			15					20					25						
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Val	Asn	Val	Gly	Gln	Asn	Leu	Val	Val	Asp	Leu	Ser	Thr	Gln	Ile	Phe				
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tgc	cat	aac	gat	tat	ccg	gaa	acc	att	aca	gac	tat	gtc	aca	ctg	caa				240
Cys	His	Asn	Asp	Tyr	Pro	Glu	Thr	Ile	Thr	Asp	Tyr	Val	Thr	Leu	Gln				
	45					50					55								
cga	ggc	tgc	gct	tat	ggc	ggc	gtg	tta	tct	aat	ttt	tcc	ggg	acc	gta				288
Arg	Gly	Ser	Ala	Tyr	Gly	Gly	Val	Leu	Ser	Asn	Phe	Ser	Gly	Thr	Val				
	60				65				70						75				
aaa	tat	agt	ggc	agt	agc	tat	cca	ttt	cct	acc	acc	agc	gaa	acg	ccg				336
Lys	Tyr	Ser	Gly	Ser	Ser	Tyr	Pro	Phe	Pro	Thr	Thr	Ser	Glu	Thr	Pro				
				80					85					90					
cgc	gtt	gtt	tat	aat	tgc	aga	acg	gat	aag	ccg	tgg	ccg	gtg	gcg	ctt				384
Arg	Val	Val	Tyr	Asn	Ser	Arg	Thr	Asp	Lys	Pro	Trp	Pro	Val	Ala	Leu				
			95					100					105						
tat	ttg	acg	cct	gtg	agc	agt	gcg	ggc	ggg	gtg	gcg	att	aaa	gct	ggc				432
Tyr	Leu	Thr	Pro	Val	Ser	Ser	Ala	Gly	Gly	Val	Ala	Ile	Lys	Ala	Gly				
		110					115					120							
tca	tta	att	gcc	gtg	ctt	att	ttg	cga	cag	acc	aac	aac	tat	aac	agc				480
Ser	Leu	Ile	Ala	Val	Leu	Ile	Leu	Arg	Gln	Thr	Asn	Asn	Tyr	Asn	Ser				
	125					130					135								

gat gat ttc cag ttt gtg tgg aat att tac gcc aat aat gat gtg gtg	528
Asp Asp Phe Gln Phe Val Trp Asn Ile Tyr Ala Asn Asn Asp Val Val	
140 145 150 155	
gtg cct act ggc ggc tgc gat gtt tct gct cgt gat gtc acc gtt act	576
Val Pro Thr Gly Gly Cys Asp Val Ser Ala Arg Asp Val Thr Val Thr	
160 165 170	
ctg ccg gac tac cct ggt tca gtg cca att cct ctt acc gtt tat tgt	624
Leu Pro Asp Tyr Pro Gly Ser Val Pro Ile Pro Leu Thr Val Tyr Cys	
175 180 185	
gcg aaa agc caa aac ctg ggg tat tac ctc tcc ggc aca acc gca gat	672
Ala Lys Ser Gln Asn Leu Gly Tyr Tyr Leu Ser Gly Thr Thr Ala Asp	
190 195 200	
gcg ggc aac tcg att ttc acc aat acc gcg tcg ttt tca cct gca cag	720
Ala Gly Asn Ser Ile Phe Thr Asn Thr Ala Ser Phe Ser Pro Ala Gln	
205 210 215	
ggc gtc ggc gta cag ttg acg cgc aac ggt acg att att cca gcg aat	768
Gly Val Gly Val Gln Leu Thr Arg Asn Gly Thr Ile Ile Pro Ala Asn	
220 225 230 235	
aac acg gta tcg tta gga gca gta ggg act tcg gcg gtg agt ctg gga	816
Asn Thr Val Ser Leu Gly Ala Val Gly Thr Ser Ala Val Ser Leu Gly	
240 245 250	
tta acg gca aat tat gca cgt acc gga ggg cag gtg act gca ggg aat	864
Leu Thr Ala Asn Tyr Ala Arg Thr Gly Gly Gln Val Thr Ala Gly Asn	
255 260 265	
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Pro Ile Gly Gly Gly Ser Ala Asn Val Tyr Val Asn Leu Ala Pro Val	
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Val Asn Val Gly Gln Asn Leu Val Val Asp Leu Ser Thr Gln Ile Phe	
30 35 40	
Cys His Asn Asp Tyr Pro Glu Thr Ile Thr Asp Tyr Val Thr Leu Gln	
45 50 55	
Arg Gly Ser Ala Tyr Gly Gly Val Leu Ser Asn Phe Ser Gly Thr Val	
60 65 70 75	
Lys Tyr Ser Gly Ser Ser Tyr Pro Phe Pro Thr Thr Ser Glu Thr Pro	
80 85 90	
Arg Val Val Tyr Asn Ser Arg Thr Asp Lys Pro Trp Pro Val Ala Leu	
95 100 105	
Tyr Leu Thr Pro Val Ser Ser Ala Gly Gly Val Ala Ile Lys Ala Gly	
110 115 120	

Ser Leu Ile Ala Val Leu Ile Leu Arg Gln Thr Asn Asn Tyr Asn Ser
125 130 135
Asp Asp Phe Gln Phe Val Trp Asn Ile Tyr Ala Asn Asn Asp Val Val
140 145 150 155
Val Pro Thr Gly Gly Cys Asp Val Ser Ala Arg Asp Val Thr Val Thr
160 165 170
Leu Pro Asp Tyr Pro Gly Ser Val Pro Ile Pro Leu Thr Val Tyr Cys
175 180 185
Ala Lys Ser Gln Asn Leu Gly Tyr Tyr Leu Ser Gly Thr Thr Ala Asp
190 195 200
Ala Gly Asn Ser Ile Phe Thr Asn Thr Ala Ser Phe Ser Pro Ala Gln
205 210 215
Gly Val Gly Val Gln Leu Thr Arg Asn Gly Thr Ile Ile Pro Ala Asn
220 225 230 235
Asn Thr Val Ser Leu Gly Ala Val Gly Thr Ser Ala Val Ser Leu Gly
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<212> DNA
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<210> 6
<211> 28
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<210> 7
<211> 48
<212> DNA
<213> Artificial

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<212> DNA
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<223> Description of Artificial Sequence: Primer

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<212> DNA
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 <210> 24
 <211> 24
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 <400> 24
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 <210> 25
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